

New computing applications expedite animal breeding

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A doctoral thesis studied new statistical methods for animal breeding, based on which extensive livestock data samples can be analysed, and complex models used, more efficiently. Computing times lasting months can be reduced to weeks.

Kaarina Matilainen, a researcher at MTT Agrifood Research Finland, explains that, in extreme cases, months of work are required to number-crunch the complex models currently used in research on animal breeding.

"I sought an efficient computing method which would enable the faster handling of data samples, using less computing capacity," says Matilainen.

Models depict livestock characteristics

In order to improve livestock, scientists need to estimate genetic parameters, such as the degree of genetic variation in certain characteristics. This is based on measurements of observed characteristics such as the milk yield in dairy cattle, or growth in pigs. Mixed models familiar from statistics can be used to assist in this, by taking account of variations arising from various sources. For every source of variation, a statistical parameter called variance has to be estimated.

Methods used to evaluate the variance parameters of models depicting animal characteristics formed the focus of the research.

"Due to the large data samples and complex models often used in [animal breeding](#) evaluations, computational efficiency tends to be a key feature of estimation methods," explains Matilainen.

The research focused on the so-called restricted maximum likelihood method. While linearisation was used to evaluate growth curves among pigs, the Monte Carlo method was used to compute variances in dairy cattle yield models. Although the methods were mainly studied using simulated data samples, genuine [dairy cattle](#) samples were also analysed.

Faster solutions for complex models

Linearisation enabled the use of existing, high-powered software with only small adjustments for growth-curve evaluation. This method worked well with data samples depicting the animals' weight development from birth to adult weight.

The new applications exploiting the Monte Carlo method proved efficient, both in terms of the computer memory required and the computing time.

"This will mean that genetic variance parameters required in animal selection programmes can be computed faster in the future. Computations that once took months will be done in just weeks," says Matilainen.

The results of her research can be used to work out more realistic and complex models within a reasonable time frame.

More information: The dissertation is available online:

jukuri.mtt.fi/bitstream/handle...ede30.pdf?sequence=6

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